



SUBSTITUTE SEQUENCE LISTING

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SEP 17 2002

TECH CENTER 1600/2900

<110> CROCE, Carlo M.
ISHII, Hideshi

<120> COMPOSITIONS, KITS, AND METHODS RELATING TO THE HUMAN
FEZ1 GENE, A NOVEL TUMOR SUPPRESSOR GENE

<130> 9855-30U1 (209855.0081)

<140> NOT YET ASSIGNED

<141> 2000-02-25

<150> US 60/121,537

<151> 1999-02-25

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<170> PatentIn Ver. 2.1

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<212> PRT

<213> Homo sapiens

<400> 4

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Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
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Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
      50              55              60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
      65              70              75              80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
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Leu	Glu	Met	Gly	Ser	Glu	Lys	Gly	Ala	Val	Arg	Pro	Thr	Ala	Phe	Lys	115	120	125
Pro	Val	Leu	Pro	Arg	Ser	Gly	Ala	Ile	Leu	His	Ser	Ser	Pro	Glu	Ser	130	135	140
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Glu	Leu	Lys	Pro	Gly	Leu	Cys	Ser	Gly	Ala	Leu	Ser	Asp	Ser	Gly	Arg	165	170	175
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Glu	Lys	Thr	Ser	Phe	Gly	Pro	Ala	Leu	Glu	Glu	Thr	Gln	Trp	Glu	Val	370	375	380
Cys	Gln	Lys	Ser	Gly	Glu	Ile	Ser	Leu	Leu	Lys	Gln	Gln	Leu	Lys	Glu	385	390	395

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 Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu
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 Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser Ala Gly Glu Pro
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 <213> Homo sapiens

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Met Ser Gly Ser Cys Gly Arg Arg Arg Arg Arg Arg
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<211> 69
<212> PRT
<213> Homo sapiens

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 <213> Homo sapiens

<400> 13						
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ctgctgaggt	ttggcttctc	ccaggactcc	ggtcacggca	agtccagctc	caaaatgggc	180
aagagcgaag	acttcttcta	catcaaggctc	agccagaaaag	cccggggctc	ccatcaccca	240
gattacacgg	cactgtccag	cggggattta	gggggcccagg	ctgggggtgga	ctttgacccg	300
tccacacccc	ccaagctcat	gcccttctcc	aatcagctag	aaatgggctc	cgagaagggg	360
gcagtgaggg	ccacagcctt	caagcctgtg	ctgccacggg	caggagccat	cctgcactcc	420
tccccggaga	gtgccagcca	ccagctgcac	cccggccctc	cagacaagcc	caaggagcag	480
gagctgaagc	ctggcctgtg	ctctggggcg	ctgtcagact	ccggccggaa	ctccatgtcc	540
agcctgcccc	cacacagcac	cagcagcagc	taccagctgg	acccgctggg	cacacccgtg	600
ggaccacaaa	gccgttttgg	gggctccgcc	cacaacatca	cccagggcat	cgtcctccag	660
gacagcaaca	tgatgagcct	gaaggctctg	tccttctccg	acggaggtag	caagctgggc	720
cactcgaaca	aggcagacaa	gggcccctcg	tgtgtccgct	ccccatctc	cacggacgag	780
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cagcgagct	ttgaggagaa	ggagcttgcc	tccagcctgg	cctacgagga	gcggccgcgg	900
cgctgcaggg	acgagctgga	gggcccggag	cccaaaggcg	gcaacaagct	caagcaggcc	960
tcgcagaaga	gccagcgcg	gcagcaggtc	ctgcacctgc	aggtactgca	gcttcagcag	1020
gagaagcggc	agctccggca	ggagctcgag	agcctcatga	aggagcagga	cctgctggag	1080
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cagtgggagg	tgtgccagaa	gtcaggcgag	atctccctcc	tgaagcagca	gctgaaggag	1200
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gacacgcggg	gcaagctgga	gggcctggag	ctgaggacct	aggacctgga	gggcgcctcg	1320
cgacccaagg	gcctggagct	ggaggtctgt	gagaatgagc	tgacgcgcaa	gaagaacgag	1380
gcggagctgc	tgccggagaa	gggtgaacctg	ctggagcggc	tgccggccga	gctgcgggag	1440
gagcggcaag	gccatgacca	gatgtcctcg	ggcttccagc	atgagcggct	cgtgtggaag	1500
gaggagaagg	agaaggtgat	tcagtaccag	aaacagctgc	agcagagcta	cgtggccatg	1560
taccagcgga	accagcgctc	ggagaaggcc	ctgcagcagc	tggcacgtgg	ggacagcgcc	1620
ggggagccct	tggaggttga	cctggaaggg	gctgacatcc	cctacgagga	catcatagcc	1680
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<210> 14
 <211> 1722
 <212> DNA
 <213> Homo sapiens

<400> 14						
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ctgctgaggt	ttggcttctc	ccaggactcc	ggtcacggca	agtccagctc	caaaatgggc	180
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gattacacgg	cactgtccag	cggggattta	gggggcccagg	ctgggggtgga	ctttgacccg	300
tccacacccc	ccaagctcat	gcccttctcc	aatcagctag	aaatgggctc	cgagaagggg	360
gcagtgaggg	ccacagcctt	caagcctgtg	ctgccacggg	caggagccat	cctgcactcc	420
tccccggaga	gtgccagcca	ccagctgcac	cccggccctc	cagacaagcc	caaggagcag	480
gagctgaagc	ctggcctgtg	ctctggggcg	ctgtcagact	ccggccggaa	ctccatgtcc	540

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agcctgcccc cacacagcac cagcagcagc taccagctgg acccgctggt cacacccgtg 600
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ctgcagcagc tggcacgtgg ggacagcgcc ggggagccct tggaggttga cctggaaggg 1680
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<210> 15
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 15
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 1 5 10 15
 His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
 20 25 30
 Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
 35 40 45
 Asp Ser Gly His Gly Lys Ala Met Thr Arg Cys Pro Arg Ala Ser Ser
 50 55 60
 Met Ser Gly Ser Cys Gly Arg Arg Arg Arg Arg Arg
 65 70 75

<210> 16
 <211> 210
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
 1 5 10 15
 His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
 20 25 30
 Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln

35					40					45					
Asp	Ser	Gly	His	Gly	Lys	Ser	Ser	Ser	Lys	Met	Gly	Lys	Ser	Glu	Asp
50						55					60				
Phe	Phe	Tyr	Ile	Lys	Val	Ser	Gln	Lys	Ala	Arg	Gly	Ser	His	His	Pro
65					70					75					80
Asp	Tyr	Thr	Ala	Leu	Ser	Ser	Gly	Asp	Leu	Gly	Gly	Gln	Ala	Gly	Val
				85					90					95	
Asp	Phe	Asp	Pro	Ser	Thr	Pro	Pro	Lys	Leu	Met	Pro	Phe	Ser	Asn	Gln
			100					105					110		
Leu	Glu	Met	Gly	Ser	Glu	Lys	Gly	Ala	Val	Arg	Pro	Thr	Ala	Phe	Lys
		115					120					125			
Pro	Val	Leu	Pro	Arg	Ser	Gly	Ala	Ile	Leu	His	Ser	Ser	Pro	Glu	Ser
	130					135					140				
Ala	Ser	His	Gln	Leu	His	Pro	Ala	Pro	Pro	Asp	Lys	Pro	Lys	Glu	Gln
145					150					155					160
Glu	Leu	Lys	Pro	Gly	Leu	Cys	Ser	Gly	Ala	Leu	Ser	Asp	Ser	Gly	Arg
				165					170					175	
Asn	Ser	Met	Ser	Ser	Leu	Pro	Thr	His	Ser	Ala	Gly	Glu	Pro	Leu	Glu
		180						185					190		
Val	Asp	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Tyr	Glu	Asp	Ile	Ile	Ala	Thr
	195						200					205			
Glu	Ile														
210															

<210> 17
 <211> 537
 <212> PRT
 <213> Homo sapiens

<400> 17															
Met	Gly	Ser	Val	Ser	Ser	Leu	Ile	Ser	Gly	His	Ser	Phe	His	Ser	Lys
1				5					10					15	
His	Cys	Arg	Ala	Ser	Gln	Tyr	Lys	Leu	Arg	Lys	Ser	Ser	His	Leu	Lys
			20					25					30		
Lys	Leu	Asn	Arg	Tyr	Ser	Asp	Gly	Leu	Leu	Arg	Phe	Gly	Phe	Ser	Gln
		35					40					45			
Asp	Ser	Gly	His	Gly	Lys	Ser	Ser	Ser	Lys	Met	Gly	Lys	Ser	Glu	Asp
	50					55					60				
Phe	Phe	Tyr	Ile	Lys	Val	Ser	Gln	Lys	Ala	Arg	Gly	Ser	His	His	Pro
65					70					75					80

Asp	Tyr	Thr	Ala	Leu	Ser	Ser	Gly	Asp	Leu	Gly	Gly	Gln	Ala	Gly	Val	85	90	95
Asp	Phe	Asp	Pro	Ser	Thr	Pro	Pro	Lys	Leu	Met	Pro	Phe	Ser	Asn	Gln	100	105	110
Leu	Glu	Met	Gly	Ser	Glu	Lys	Gly	Ala	Val	Arg	Pro	Thr	Ala	Phe	Lys	115	120	125
Pro	Val	Leu	Pro	Arg	Ser	Gly	Ala	Ile	Leu	His	Ser	Ser	Pro	Glu	Ser	130	135	140
Ala	Ser	His	Gln	Leu	His	Pro	Ala	Pro	Pro	Asp	Lys	Pro	Lys	Glu	Gln	145	150	155
Glu	Leu	Lys	Pro	Gly	Leu	Cys	Ser	Gly	Ala	Leu	Ser	Asp	Ser	Gly	Arg	165	170	175
Asn	Ser	Met	Ser	Ser	Leu	Pro	Thr	His	Ser	Thr	Ser	Ser	Ser	Tyr	Gln	180	185	190
Leu	Asp	Pro	Leu	Val	Thr	Pro	Val	Gly	Pro	Thr	Ser	Arg	Phe	Gly	Gly	195	200	205
Ser	Ala	His	Asn	Ile	Thr	Gln	Gly	Ile	Val	Leu	Gln	Asp	Ser	Asn	Met	210	215	220
Met	Ser	Leu	Lys	Ala	Leu	Ser	Phe	Ser	Asp	Gly	Gly	Ser	Lys	Leu	Gly	225	230	235
His	Ser	Asn	Lys	Ala	Asp	Lys	Gly	Pro	Ser	Cys	Val	Arg	Ser	Pro	Ile	245	250	255
Ser	Thr	Asp	Glu	Cys	Ser	Ile	Gln	Glu	Leu	Glu	Gln	Lys	Leu	Leu	Glu	260	265	270
Arg	Glu	Gly	Ala	Leu	Gln	Lys	Leu	Gln	Arg	Ser	Phe	Glu	Glu	Lys	Glu	275	280	285
Leu	Ala	Ser	Ser	Leu	Ala	Tyr	Glu	Glu	Arg	Pro	Arg	Arg	Cys	Arg	Asp	290	295	300
Glu	Leu	Glu	Gly	Pro	Glu	Pro	Lys	Gly	Gly	Asn	Lys	Leu	Lys	Gln	Ala	305	310	315
Ser	Gln	Lys	Ser	Gln	Arg	Ala	Gln	Gln	Val	Leu	His	Leu	Gln	Val	Leu	325	330	335
Gln	Leu	Gln	Gln	Glu	Lys	Arg	Gln	Leu	Arg	Gln	Glu	Leu	Glu	Ser	Leu	340	345	350
Met	Lys	Glu	Gln	Asp	Leu	Leu	Glu	Thr	Lys	Leu	Arg	Ser	Tyr	Glu	Arg	355	360	365
Glu	Lys	Thr	Ser	Phe	Gly	Pro	Ala	Leu	Glu	Glu	Thr	Gln	Trp	Glu	Val	370	375	380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu
 385 390 395 400
 Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys
 405 410 415
 Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg
 420 425 430
 Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu
 435 440 445
 Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu
 450 455 460
 Arg Glu Lys His Glu Arg Leu Val Trp Lys Glu Glu Lys Glu Lys Val
 465 470 475 480
 Ile Gln Tyr Gln Lys Gln Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln
 485 490 495
 Arg Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp
 500 505 510
 Ser Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro
 515 520 525
 Tyr Glu Asp Ile Ile Ala Thr Glu Ile
 530 535

<210> 18
 <211> 504
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
 1 5 10 15
 His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
 20 25 30
 Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
 35 40 45
 Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
 50 55 60
 Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
 65 70 75 80
 Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
 85 90 95
 Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln

100					105					110						
Leu	Glu	Met	Gly	Ser	Glu	Lys	Gly	Ala	Val	Arg	Pro	Thr	Ala	Phe	Lys	
115					120					125						
Pro	Val	Leu	Pro	Arg	Ser	Gly	Ala	Ile	Leu	His	Ser	Ser	Pro	Glu	Ser	
130					135					140						
Ala	Ser	His	Gln	Leu	His	Pro	Ala	Pro	Pro	Asp	Lys	Pro	Lys	Glu	Gln	
145					150					155					160	
Glu	Leu	Lys	Pro	Gly	Leu	Cys	Ser	Gly	Ala	Leu	Ser	Asp	Ser	Gly	Arg	
165					170					175						
Asn	Ser	Met	Ser	Ser	Leu	Pro	Thr	His	Ser	Thr	Ser	Ser	Ser	Tyr	Gln	
180					185					190						
Leu	Asp	Pro	Leu	Val	Thr	Pro	Val	Gly	Pro	Thr	Ser	Arg	Phe	Gly	Gly	
195					200					205						
Ser	Ala	His	Asn	Ile	Thr	Gln	Gly	Ile	Val	Leu	Gln	Asp	Ser	Asn	Met	
210					215					220						
Met	Ser	Leu	Lys	Ala	Leu	Ser	Phe	Ser	Asp	Gly	Gly	Ser	Lys	Leu	Gly	
225					230					235					240	
His	Ser	Asn	Lys	Ala	Asp	Lys	Gly	Pro	Ser	Cys	Val	Arg	Ser	Pro	Ile	
245					250					255						
Ser	Thr	Asp	Glu	Cys	Ser	Ile	Gln	Glu	Leu	Glu	Gln	Lys	Leu	Leu	Glu	
260					265					270						
Arg	Glu	Gly	Ala	Leu	Gln	Lys	Leu	Gln	Arg	Ser	Phe	Glu	Glu	Lys	Glu	
275					280					285						
Leu	Ala	Ser	Ser	Leu	Ala	Tyr	Glu	Glu	Arg	Pro	Arg	Arg	Cys	Arg	Asp	
290					295					300						
Glu	Leu	Glu	Gly	Pro	Glu	Pro	Lys	Gly	Gly	Asn	Lys	Leu	Lys	Gln	Ala	
305					310					315					320	
Ser	Gln	Lys	Ser	Gln	Arg	Ala	Gln	Gln	Val	Leu	His	Leu	Gln	Val	Leu	
325					330					335						
Gln	Leu	Gln	Gln	Glu	Lys	Arg	Gln	Leu	Arg	Gln	Glu	Leu	Glu	Ser	Leu	
340					345					350						
Met	Lys	Glu	Gln	Asp	Leu	Leu	Glu	Thr	Lys	Leu	Arg	Ser	Tyr	Glu	Arg	
355					360					365						
Glu	Lys	Thr	Ser	Phe	Gly	Pro	Ala	Leu	Glu	Glu	Thr	Gln	Trp	Glu	Val	
370					375					380						
Cys	Gln	Lys	Ser	Gly	Glu	Ile	Ser	Leu	Leu	Lys	Gln	Gln	Leu	Lys	Glu	
385					390					395					400	
Ser	Gln	Thr	Glu	Val	Asn	Ala	Lys	Ala	Ser	Glu	Ile	Leu	Gly	Leu	Lys	

Glu	Leu	Lys	Pro	Gly	Leu	Cys	Ser	Gly	Ala	Leu	Ser	Asp	Ser	Gly	Arg	
				165					170					175		
Asn	Ser	Met	Ser	Ser	Leu	Pro	Thr	His	Ser	Thr	Ser	Ser	Ser	Tyr	Gln	
			180					185						190		
Leu	Asp	Pro	Leu	Val	Thr	Pro	Val	Gly	Pro	Thr	Ser	Arg	Phe	Gly	Gly	
		195					200					205				
Ser	Ala	His	Asn	Ile	Thr	Gln	Gly	Ile	Val	Leu	Gln	Asp	Ser	Asn	Met	
	210					215					220					
Met	Ser	Leu	Lys	Ala	Leu	Ser	Phe	Ser	Asp	Gly	Gly	Ser	Lys	Leu	Gly	
225					230					235					240	
His	Ser	Asn	Lys	Ala	Asp	Lys	Gly	Pro	Ser	Cys	Val	Arg	Ser	Pro	Ile	
			245					250						255		
Ser	Thr	Asp	Glu	Cys	Ser	Ile	Gln	Glu	Leu	Glu	Gln	Lys	Leu	Leu	Glu	
			260					265					270			
Arg	Glu	Gly	Ala	Leu	Gln	Lys	Leu	Gln	Arg	Ser	Phe	Glu	Glu	Lys	Glu	
		275					280					285				
Leu	Ala	Ser	Ser	Leu	Ala	Tyr	Glu	Glu	Arg	Pro	Arg	Arg	Cys	Arg	Asp	
	290					295				300						
Glu	Leu	Glu	Gly	Pro	Glu	Pro	Lys	Gly	Gly	Asn	Lys	Leu	Lys	Gln	Ala	
305					310					315					320	
Ser	Gln	Lys	Ser	Gln	Arg	Ala	Gln	Gln	Val	Leu	His	Leu	Gln	Val	Leu	
				325					330					335		
Gln	Leu	Gln	Gln	Glu	Lys	Arg	Gln	Leu	Arg	Gln	Glu	Leu	Glu	Ser	Leu	
			340					345					350			
Met	Lys	Glu	Gln	Asp	Leu	Leu	Glu	Thr	Lys	Leu	Arg	Ser	Tyr	Glu	Arg	
		355					360					365				
Glu	Lys	Thr	Ser	Phe	Gly	Pro	Ala	Leu	Glu	Glu	Thr	Gln	Trp	Glu	Val	
	370					375					380					
Cys	Gln	Lys	Ser	Gly	Glu	Ile	Ser	Leu	Leu	Lys	Gln	Gln	Leu	Lys	Glu	
385					390					395					400	
Ser	Gln	Thr	Glu	Val	Asn	Ala	Lys	Ala	Ser	Glu	Ile	Leu	Gly	Leu	Lys	
				405					410					415		
Ala	Gln	Leu	Lys	Asp	Thr	Arg	Gly	Lys	Leu	Glu	Gly	Leu	Glu	Leu	Arg	
			420					425					430			
Thr	Gln	Asp	Leu	Glu	Gly	Ala	Leu	Arg	Thr	Lys	Gly	Leu	Glu	Leu	Glu	
		435					440					445				
Val	Cys	Glu	Asn	Glu	Leu	Gln	Arg	Lys	Lys	Asn	Glu	Ala	Glu	Leu	Leu	
	450					455					460					

Arg Glu Lys Val Asn Leu Leu Glu Arg Leu Arg Ala Glu Leu Arg Glu
 465 470 475 480
 Glu Arg Gln Gly His Asp Gln Met Ser Ser Gly Phe Gln His Glu Arg
 485 490 495
 Leu Val Trp Lys Glu Glu Lys Glu Lys Val Ile Gln Tyr Gln Lys Gln
 500 505 510
 Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg Asn Gln Arg Leu Glu
 515 520 525
 Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser Ala Gly Glu Pro Leu
 530 535 540
 Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala
 545 550 555 560
 Thr Glu Ile

<210> 20
 <211> 573
 <212> PRT
 <213> Homo sapiens

<400> 20
 Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
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 His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
 20 25 30
 Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
 35 40 45
 Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp
 50 55 60
 Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro
 65 70 75 80
 Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val
 85 90 95
 Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln
 100 105 110
 Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys
 115 120 125
 Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser
 130 135 140
 Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln

145		150		155		160									
Glu	Leu	Lys	Pro	Gly	Leu	Cys	Ser	Gly	Ala	Leu	Ser	Asp	Ser	Gly	Arg
				165					170					175	
Asn	Ser	Met	Ser	Ser	Leu	Pro	Thr	His	Ser	Thr	Ser	Ser	Ser	Tyr	Gln
			180					185						190	
Leu	Asp	Pro	Leu	Val	Thr	Pro	Val	Gly	Pro	Thr	Ser	Arg	Phe	Gly	Gly
		195					200					205			
Ser	Ala	His	Asn	Ile	Thr	Gln	Gly	Ile	Val	Leu	Gln	Asp	Ser	Asn	Met
	210					215					220				
Met	Ser	Leu	Lys	Ala	Leu	Ser	Phe	Ser	Asp	Gly	Gly	Ser	Lys	Leu	Gly
225					230					235					240
His	Ser	Asn	Lys	Ala	Asp	Lys	Gly	Pro	Ser	Cys	Val	Arg	Ser	Pro	Ile
				245					250					255	
Ser	Thr	Asp	Glu	Cys	Ser	Ile	Gln	Glu	Leu	Glu	Gln	Lys	Leu	Leu	Glu
			260					265					270		
Arg	Glu	Gly	Ala	Leu	Gln	Lys	Leu	Gln	Arg	Ser	Phe	Glu	Glu	Lys	Glu
		275					280					285			
Leu	Ala	Ser	Ser	Leu	Ala	Tyr	Glu	Glu	Arg	Pro	Arg	Arg	Cys	Arg	Asp
	290					295					300				
Glu	Leu	Glu	Gly	Pro	Glu	Pro	Lys	Gly	Gly	Asn	Lys	Leu	Lys	Gln	Ala
305					310					315					320
Ser	Gln	Lys	Ser	Gln	Arg	Ala	Gln	Gln	Val	Leu	His	Leu	Gln	Val	Leu
				325					330					335	
Gln	Leu	Gln	Gln	Glu	Lys	Arg	Gln	Leu	Arg	Gln	Glu	Leu	Glu	Ser	Leu
			340					345					350		
Met	Lys	Glu	Gln	Asp	Leu	Leu	Glu	Thr	Lys	Leu	Arg	Ser	Tyr	Glu	Arg
		355					360					365			
Glu	Lys	Thr	Ser	Phe	Gly	Pro	Ala	Leu	Glu	Glu	Thr	Gln	Trp	Glu	Val
		370				375					380				
Cys	Gln	Lys	Ser	Gly	Glu	Ile	Ser	Leu	Leu	Lys	Gln	Gln	Leu	Lys	Glu
385					390					395					400
Ser	Gln	Thr	Glu	Val	Asn	Ala	Lys	Ala	Ser	Glu	Ile	Leu	Gly	Leu	Lys
				405					410					415	
Ala	Gln	Leu	Lys	Asp	Thr	Arg	Gly	Lys	Leu	Glu	Gly	Leu	Glu	Leu	Arg
			420					425					430		
Thr	Gln	Asp	Leu	Glu	Gly	Ala	Leu	Arg	Thr	Lys	Gly	Leu	Glu	Leu	Glu
		435					440					445			
Val	Cys	Glu	Asn	Glu	Leu	Gln	Arg	Lys	Lys	Asn	Glu	Ala	Glu	Leu	Leu

450	455	460
Arg Glu Lys Val Asn Leu Leu Glu Gln Glu Leu Gln Glu Leu Arg Ala		
465	470	475 480
Gln Ala Ala Leu Ala Arg Asp Met Gly Pro Pro Thr Phe Pro Glu Asp		
485	490	495
Val Pro Ala Leu Gln Arg Glu Leu Glu Arg Leu Val Trp Lys Glu Glu		
500	505	510
Lys Glu Lys Val Ile Gln Tyr Gln Lys Gln Leu Gln Gln Ser Tyr Val		
515	520	525
Ala Met Tyr Gln Arg Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu		
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Ala Arg Gly Asp Ser Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly		
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565	570	

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<210> 22
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 region amplificatin primer G12

<400> 22
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<210> 23
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 region amplification primer G13

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 region amplification primer G14.2

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 region amplification primer G15

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 <210> 26
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 region amplification primer G16

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 <210> 27
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region amplification primer IntABR

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<210> 28

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<212> DNA

<213> Artificial Sequence

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21

<210> 29

<211> 22

<212> DNA

<213> Artificial Sequence

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region amplification primer G17

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<212> DNA

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region amplification primer G20

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<210> 31

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<212> DNA

<213> Artificial Sequence

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region amplification primer G21

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region amplification primer G32

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<210> 33
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region amplification primer IntBCR

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<210> 34
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region amplification primer IntBCF

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<210> 35
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region amplification primer Mut6

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<210> 36

<211> 23
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 region amplification primer G1

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 <210> 37
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 region amplification primer G2

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 <210> 38
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 region amplification primer G75

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 region amplification primer G82

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 <210> 40
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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G5

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<210> 41

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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G6

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<210> 42

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G7

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<210> 43

<211> 22

<212> DNA

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<223> Description of Artificial Sequence: FEZ1 alterable
region amplification primer G8

<400> 43

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<210> 44

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: First strand
of partially-double stranded adapter-linker

<400> 44

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24

<210> 45
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<220>
<223> Description of Artificial Sequence: Second strand
of partially-double stranded adapter-linker

<400> 45
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<210> 46
<211> 23
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sequence of truncated FEZ1 truncation region

<400> 46
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<210> 47
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<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 47
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<210> 48
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sequence of truncated FEZ1 truncation region

<400> 48
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<210> 49
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<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 49

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21

<210> 50

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

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gtgagaatga gctgcagcgc aag

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<210> 51

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 51

cagcagagct acgtggccat gt

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<210> 52

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

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<210> 53

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 53
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<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 54
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<210> 55
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<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 55
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<210> 56
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<223> Description of Artificial Sequence: Donor site
sequence of truncated FEZ1 truncation region

<400> 56
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<210> 57
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acceptor site
sequence of truncated FEZ1 truncation region

<400> 57
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<210> 58
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer for
amplifying FEZ1 cDNA

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cagatgggca gcgtcagtag cctcatc

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<210> 59
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<223> Description of Artificial Sequence: Primer for
amplifying FEZ1 cDNA

<400> 59
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<210> 60
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sequence of vector pQBI-AdCMV5-IRES-GFP

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